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<150> JP 2003-379114

<151> 2003. 11. 7

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<170> PatentIn Ver. 3.1

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Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser				
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ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg			2475	
Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala				
580	585	590		
tta tca tgg gaa ttt gga tac cca gaa gta aaa cct agt gat aac tgg			2523	
Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp				
595	600	605		
gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt			2571	
Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly				
610	615	620	625	
gaa aat gat tat gta act ttt gat ttc tat cta gat cca gtt cgt gca			2619	
Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala				
630	635	640		
aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac			2667	
Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn				
645	650	655		
ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa			2715	
Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu				
660	665	670		
tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa			2763	
Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys				
675	680	685		
att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt			2811	
Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg				
690	695	700	705	
aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga			2859	
Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg				
710	715	720		
gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg			2907	
Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro				
725	730	735		
gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat			2955	
Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp				
740	745	750		
gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa			3003	
Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys				
755	760	765		
gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca			3051	
Glu Ala Val Lys Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala				
770	775	780	785	
atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct			3105	

aaaggctcga tgcagatctt ttagataacc ttttttgca taactggaca tagaatggtt 3165
attaaagaaa gcaagggttt tatacgatat taaaaaggta gcgatitaa attgaaacct 3225
ttaataatgt ctgtgtatag aatgtatgaag taatttaaga gggggaaacg aagtgaaaac 3285
ggaaatitct agtataagaa aaacagacca agaaatactg caagct 3332

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-10 -5 -1 1

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
5 10 15

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
20 25 30 35

Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
40 45 50

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
55 60 65

Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile Arg Leu
70 75 80

Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu Leu Ile
85 90 95

Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn Asp Met
100 105 110 115

Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
120 125 130

Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala Ala Leu
135 140 145

Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser
150 155 160

Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
165 170 175

Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Asp
180 185 190 195

Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
200 205 210

Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
215 220 225

Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr
230 235 240

Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met
245 250 255

Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr
260 265 270 275

Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr Phe Asp
280 285 290

Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp
295 300 305

Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr
310 315 320

Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp Pro Gly Pro
325 330 335

Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val
340 345 350 355

Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys
360 365 370

Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe
375 380 385

Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu Asn Glu
390 395 400

Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp Val Ser
405 410 415

Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly Trp Gly
420 425 430 435

Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val Ile
440 445 450

Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln Gly Pro
455 460 465

Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu Pro Thr
470 475 480

Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr Ile Thr
 485 490 495

Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala Glu Asn
 500 505 510 515

Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly Ala Asp
 520 525 530

Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile
 535 540 545

Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe
 550 555 560

Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val
 565 570 575

Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser
 580 585 590 595

Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr
 600 605 610

Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn
 615 620 625

Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu
 630 635 640

Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr
 645 650 655

Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu
 660 665 670 675

Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn
 680 685 690

Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met
 695 700 705

Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe
 710 715 720

Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu
 725 730 735

Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys
 740 745 750 755

Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala
 760 765 770

Val Ly**WO 2005/045045** Lys Glu Ala Lys Glu Glu Lys Lys Ala Ile Lys
775 780 785

PCT/JP2004/016890

Asn Glu Ala Thr Lys Lys
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<400> 6
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acg atg atg cag tat tat gag tgg cat ttg gaa aac gac ggg cag cat 690
 Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp Gly Gln His
 10 15 20

tgg aat cg²⁵ t³⁰ g³⁵ cac gat gat gcc gca gct t⁷³⁸ t⁷³⁸
Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu Ser Asp Ala Gly Ile

aca gct att tgg att ccg cca gcc tac aaa ggt aat agt cag gcg gat 786
 Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser Gln Ala Asp
 40 45 50

gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag ttc aat caa 834
 Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Asn Gln
 55 60 65

aag ggt act gtt cga acg aaa tac gga act aag gca cag cit gaa cga	882
Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Leu Glu Arg	
70 75 80 85	

gct atc WO 2005/045045 taa tct aat gat atc aat gta tac gga gat gtc Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr Gly Asp Val 90 95 100	930	PCT/JP2004/016890
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acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt aac aac gcc Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg Asn Asn Ala 135 140 145	1074	
tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt gtt gac tgg Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly Val Asp Trp 150 155 160 165	1122	
gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca aat acg aac Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala Asn Thr Asn 170 175 180	1170	
tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat tac ctg tta Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp Tyr Leu Leu 185 190 195	1218	
gga tcg aat atc gac ttt agt cat cca gaa gta caa gat gag ttg aag Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp Glu Leu Lys 200 205 210	1266	
gat tgg ggt agc tgg ttt acc gat gag tta gat ttg gat ggt tat cgt Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp Leu Asp Gly Tyr Arg 215 220 225	1314	
tta gat gct att aaa cat att cca ttc tgg tat aca tct gat tgg gtt Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr Thr Ser Asp Trp Val 230 235 240 245	1362	
cgg cat cag cgc aac gaa gca gat caa gat tta ttt gtc gta ggg gaa Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu Phe Val Val Gly Glu 250 255 260	1410	
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aat tgg gag atg tct cta ttc gat gtt cca ctt aat tat aat ttt tac Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu Asn Tyr Asn Phe Tyr 280 285 290	1506	
cgg gct tca caa caa ggt gga agc tat gat atg cgt aat att tta cga Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met Arg Asn Ile Leu Arg 295 300 305	1554	
gga tct tta gta gaa gcg cat ccg atg cat gca gtt acg ttt gtt gat Gly Ser Leu Val Glu Ala His Pro Met His Ala Val Thr Phe Val Asp 310 315 320 325	1602	
aat cat gat act cag cca ggg gag tca tta gag tca tgg gtt gct gat Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu Ser Trp Val Ala Asp 330 335 340	1650	
tgg ttt aag cca ctt gct tat gcg aca att ttg acg cgt gaa ggt ggt Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu Thr Arg Glu Gly Gly 345 350 355	1698	
aat cca aat gta ttt tac ggt gat tac tat ggg att cct aac gat aac Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro Asn Asp Asn 360 365 370	1746	
att tca gct aaa aaa gat atg att gat gag ctg ctt gat gca cgt caa	1794	

Ile Ser WO 2005/045045 sp Met Ile Asp Glu Leu Leu Asp Ala Arg Gln
375 380 385

PCT/JP2004/016890

aat tac gca tat ggc acg cag cat gac tat ttt gat cat tgg gat gtt 1842
Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His Trp Asp Val
390 395 400 405

gta gga tgg act agg gaa gga tct tcc tcc aga cct aat tca ggc ctt 1890
Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg Pro Asn Ser Gly Leu
410 415 420

gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg atg tat gta 1938
Ala Thr Ile Met Ser Asn Gly Pro Gly Ser Lys Trp Met Tyr Val
425 430 435

gga cgt cag aat gca gga caa aca tgg aca gat ita act ggt aat aac 1986
Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr Gly Asn Asn
440 445 450

gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa ttc ttt acg 2034
Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu Phe Phe Thr
455 460 465

aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaag ctttggaaag 2087
Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
470 475 480

ggattccccc ctaactcaag gctttcttta tgcgccttag cttacgctt ctacgacttt 2147
gaagcttggg gatccgtcga gacaaggtaa aggataaaac agcacaattc caagaaaaac 2207
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<212> PRT

<213> Bacillus sp. pHSP-K38

<400> 22

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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Leu
20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

Val Tyr Asp Val Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

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Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225 230 235 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
260 265 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
275 280 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Ser Tyr Asp Met
290 295 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465 470 475 480